IN THE CLAIMS

As set forth below, please amend claims 27, 40, and 41, and cancel claim 39.

1-19. (Cancelled)

20. (Previously presented) A method for identifying transduced mammalian hematopoietic cells comprising:

a) retrovirally transducing mammalian hematopoietic cells with a nucleic acid sequence encoding a mutated epidermal growth factor receptor (EGFR) operatively linked to an expression control sequence, wherein said mutated EGFR comprises modifications to the intracellular and the extracellular domains, comprises a modification to the extracellular domain, or comprises a modification to the intracellular domain;

b) incubating the transduced mammalian hematopoietic cells with a marked antibody which recognizes and binds specifically to the mutated EGFR; and

c) identifying the marked transduced mammalian hematopoietic cells.

21-22. (Cancelled)

23. (Previously presented) The method according to claim 20, wherein the mammalian hematopoietic cells are transduced by a retroviral vector selected from the group consisting of a moloney murine leukemia viral vector, a myeloproliferative sarcoma viral vector, a murine embryonic stem cell viral vector, a murine stem cell viral vector, and a spleen focus forming viral vector.

24. (Previously presented) The method according to claim 20, wherein the mammalian hematopoietic cells are transduced by a lentiviral vector.

25. (Previously presented) The method according to claim 20, further comprising the step of separating the identified marked transduced mammalian hematopoietic cells from non-marked mammalian hematopoietic cells.

26. (Previously presented) The method according to claim 20, further comprising the step of expanding the marked transduced mammalian hematopoietic cells.

27. (Currently amended) A method of identifying mammalian hematopoietic cells expressing a protein of interest, comprising:

a) introducing into a mammalian hematopoietic cell a nucleic acid comprising a DNA sequence encoding a protein of interest and comprising a DNA sequence encoding a mutated epidermal growth factor receptor 1 (EGFR1), ~~(EGFR),~~ wherein said DNA sequences are operatively linked to one or more expression control sequences, and wherein said mutated EGFR1 ~~EGFR~~ comprises modifications to the intracellular and the extracellular domains, comprises a modification to the extracellular domain, or comprises a modification to the intracellular domain;

b) culturing the resulting mammalian hematopoietic cells; and

c) identifying mammalian hematopoietic cells which express the mutated EGFR1 ~~EGFR~~ thereby obtaining mammalian hematopoietic cells which express the protein of interest.

28. (Cancelled)

29. (Previously presented) The method according to claim 27, wherein the nucleic acid is introduced by a retroviral vector.

30-35. (Cancelled)

36. (Previously presented) The method according to claim 20, wherein the mutated EGFR is a mutated EGFR1.

37. (Previously presented) The method according to claim 36, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 679-1210 are deleted.

38. (Previously presented) The method according to claim 36, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 25-312 and 679-1210 are deleted.

39. (Cancelled)

40. (Currently amended) The method according to claim 27 ~~39~~, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 679-1210 are deleted.

41. (Currently amended) The method according to claim 27 ~~39~~, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 25-312 and 679-1210 are deleted.

42. (Previously presented) A method of identifying a genetically modified mammalian cell, comprising:

a) introducing a nucleic acid sequence encoding a mutated epidermal growth factor receptor 1 (EGFR1), operatively linked to an expression control sequence, into a mammalian cell to form a genetically modified mammalian cell, wherein the mutated EGFR1 either comprises: i) the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 679-1210 are deleted, or ii) the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 25-312 and 679-1210 are deleted;

b) allowing expression of the mutated EGFR1 in the genetically modified mammalian cell; and

c) identifying said genetically modified mammalian cell expressing the mutated EGFR1.

43. (Previously presented) The method according to claim 42, wherein the introducing step is accomplished by incorporating the nucleic acid sequence encoding the mutated EGFR1 into a vector and introducing said vector into said mammalian cell.

44. (Previously presented) The method according to claim 43, wherein the vector is a retroviral vector.

45. (Previously presented) The method according to claim 42, further comprising separating the identified cell expressing the mutated EGFR1.

46. (Previously presented) The method according to claim 42, wherein the mammalian cell is a human cell.

47. (Previously presented) The method according to claim 46, wherein the human cell is selected from the group consisting of a hematopoietic cell, a liver cell, an endothelial cell and a smooth muscle cell.

48. (Previously presented) The method according to claim 46, wherein the human cell is a hematopoietic cell.

49. (Previously presented) The method according to claim 48, wherein the hematopoietic cell is a stem cell or T-cell.

50. (Previously presented) The method according to claim 43, wherein a heterologous coding sequence is also incorporated into said vector.

51. (Previously presented) The method according to claim 42, wherein the identifying step is accomplished by contacting the genetically modified mammalian cell with an antibody that recognizes and binds to the mutated EGFR1.

52. (Previously presented) A method of identifying a genetically modified cell, comprising:

a) introducing into a cell a nucleic acid sequence encoding a mutated epidermal growth factor receptor (EGFR), operatively linked to an expression control sequence, to form a genetically modified cell, wherein said cell is a human hematopoietic cell, a human liver cell, a human endothelial cell, or a human smooth muscle cell, and wherein said mutated EGFR comprises modifications to the intracellular and the extracellular

domains, comprises a modification to the extracellular domain, or comprises a modification to the intracellular domain;

b) allowing expression of the mutated EGFR in the genetically modified cell; and

c) identifying said genetically modified cell expressing the mutated EGFR.

53. (Previously presented) The method according to claim 52, wherein the cell is a human hematopoietic cell.

54. (Previously presented) The method according to claim 53, wherein the human hematopoietic cell is a stem cell or T-cell.

55. (Previously presented) The method according to claim 52, wherein the mutated EGFR is a mutated EGFR1.

56. (Previously presented) The method according to claim 55, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 679-1210 are deleted.

57. (Previously presented) The method according to claim 55, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 25-312 and 679-1210 are deleted.

58. (Previously presented) The method according to claim 52, wherein the introducing step is accomplished by incorporating the nucleic acid sequence encoding the mutated EGFR into a vector and introducing said vector into said cell.

59. (Previously presented) The method according to claim 58, wherein the vector is a retroviral vector.

60. (Previously presented) The method according to claim 52, further comprising separating the identified cell expressing the mutated EGFR.

61. (Previously presented) The method according to claim 58, wherein a heterologous coding sequence is also incorporated into said vector.

62. (Previously presented) The method according to claim 52, wherein the identifying step is accomplished by contacting the genetically modified cell with an antibody that recognizes and binds to the mutated EGFR.

63. (Previously presented) A method for identifying transduced mammalian cells comprising:

a) transducing mammalian cells with a lentiviral vector comprising a nucleic acid sequence encoding a mutated epidermal growth factor receptor (EGFR) operatively linked to an expression control sequence, wherein said mutated EGFR comprises modifications to the intracellular and the extracellular domains, comprises a modification to the extracellular domain, or comprises a modification to the intracellular domain;

b) incubating the transduced mammalian cells with a marked antibody which recognizes and binds specifically to the mutated EGFR; and

c) identifying the marked transduced mammalian cells.

64. (Previously presented) The method according to claim 63, wherein the mutated EGFR is a mutated EGFR1.

65. (Previously presented) The method according to claim 64, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 679-1210 are deleted.

66. (Previously presented) The method according to claim 64, wherein the mutated EGFR1 comprises the amino acid sequence set forth in SEQ ID NO:2 except that amino acid residues 25-312 and 679-1210 are deleted.

67. (Previously presented) The method according to claim 63, wherein the mammalian cells are human cells.

68. (Previously presented) The method according to claim 67, wherein the human cells are selected from the group consisting of hematopoietic cells, liver cells, endothelial cells and smooth muscle cells.

69. (Previously presented) The method according to claim 67, wherein the human cells are hematopoietic cells.

70. (Previously presented) The method according to claim 69, wherein the hematopoietic cells are stem cells or T-cells.

71. (Previously presented) The method according to claim 63, wherein said lentiviral vector also comprises a nucleic acid sequence encoding a heterologous protein of interest.

72. (Previously presented) The method according to claim 63, wherein the identifying step is accomplished by contacting the genetically modified mammalian cell with an antibody that recognizes and binds to the mutated EGFR.